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Figure 1A

Synthetic Oligonucleotide DNA Family Encoding Anti-Green Flourescent Protein Ribozymes

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3GA-		GGA	CAG- GTC-	ACC	ACT	GAA	AGC	AGA
ACCAGGA-3 TGGTCCT-5	ACGTCGC-3 TGCAGCG-5	ACACGCT-3 TGTGCGA-5	ACTTCAG-3 TGAAGTC-5	AGGGTGG-3 TCCCACC-5	AGGCACT - 3 TCCGTGA - 5	ACTTGAA - 3 TGAACTT - 5	ACGTAGC-3 TGCATCG-5	AAGAAGA-3 TTCTTCT-5
GAA A	GAA A	GAA P	GAA 7	GAA 7	GAA /	GAA /	GAA /	GAA
GAC	GAC	GAC	GAC	GAC	GAC	GAC	GAC	GAC
GAC	GAC	GAC	GAC	GAC	GAC	GAC	GAC	GAC
GAG	GAG	GAG	GAG	GAG	GAG	GAG	GAG	GAG
CGT (GCA (CGT C	CGT (CGT	CGT	CGT	CGT		
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GTC	GTC	GTC	GTC	GTC	GTC	GTC	GTC CGT	GTC CGT
TGA	TGA ACT	TGA	TGA	TGA	TGA	TGA	TGA	TGA
C TGA G ACT	C TGA G ACT	C TGA	C TGA	C TGA	C TGA G ACT	C TGA G ACT	C TGA G ACT	C TGA G ACT
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T.C.		500	AC	-TGGTCAC	-AGCGGCT -TCGCCGA	-CATGGCG	-GCTCCTG -CGAGGAC	-CGTCCTT -GCAGGAA
AGC TCG	360	900	AGA	CAC	999	ACC	TC	TC(
-CCAGCTC	-GGCCGTT	-cTcGccG -GAGCGGC	-GCAGATG -CGTCTAC	-TG	-AG	45-	၁၁ ၅	99-
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Figure 1B

Synthetic Oligonucleotide DNA Family Encoding Anti-Green Flourescent Protein Ribozymes

AACTTCA-3' TTGAAGT-5'	ACCAGGG-3' TGGTCCC-5'	AAGTCGA-3' TTCAGCT-5'	ACTCCAG-3' TGAGGTC-5'	ACGTTGT-3' TGCAACA-5'	AAGTTCA-3' TTCAAGT-5'	AGCTGCA-3' TCGACGT-5'	ACGGGGC-3' TGCCCCG-5'	TGA GTC CGT GAG GAC GAA ACTGGGT-3'	The latest the second district to the latest territories and the latest ter
GAA									
GAC CTG	GAC (CTG (GAC (CTG (GAC (CTG	GAC	GAC			GAC	
GAC G	GAC G	GAC G	GAC C	GAC C	GAC (CTG (GAC GAC	GAC GAC	GAC CTG	
GAG G	GAG (CTC (GAG (CTC (GAG (CTC (GAG			GAG	GAG	
CGT C	GCA	CGT	CGT	CGT	CGT	GTC CGT GAG	GTC CGT	CGT	
GTC									
TGA	TGA	TGA	TGA ACT	TGA	TGA	TGA ACT	TGA	TGA ACT	
C TGA G ACT	C TGA	C TGA G ACT	TGA						
טט	טט	טט	0 0	ပေဖ	ပဗ	ပဗ	ပေဖ	ပဗ	
-ceccerc	-TGCGGTT	-CCTCCTT	-GTAGTTG -CATCAAC	-TGATATA -ACTATAT	-GGATCTT -CCTAGAA	-GGTCGGC -CCAGCCG	-GCAGCAG -CGTCGTC	-CAGGGCG C TGA TGA -GTCCCGC G ACT ACT	
	3.5	3.5	3.1	3.5	3.	3.1	-0 ·ε	3.5	
10)	11)	12)	13)	14)	15)	16)	17)	18)	

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Figure 1C

Synthetic Oligonucleotide DNA Family Encoding Anti-Green Flourescent Protein Ribozymes

GAA ACCATGT-3'	AGAGTGA-3' TCTCACT-5'
GAA	GAA
GAC CTG	GAC
GAC	GAC
GAG	GAG
CGT	CGT
GTC	GTC
TGA GTC ACT CAG	TGA
FGA TGA	TGA
FGA TGA	TGA
FGA TGA	TGA
TGA	

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TCA GCT GGG	AGA ATT CGG
TCA T	TCA A
TCA	TCA
225	CCC
ACT	ACT
ATC	ATC
299	GGC
TTC	TTC
ACT	CTT
AGT	AAG
pGEM-Sca/Pvu	pGEM-oligo1/3

pGEMEX-Sma/Kpn	GCC A <u>GT ACC</u> GAT GGA GGC CGG T <u>CA TGG</u> GCT ACT CCG	AGT	ACC	GAT	GGA	999 000	AGT TCA	GAT	CGG	GAA	3C AGT GAT GCC GAA CCC GGG GGC CCG	222	GGC	വള വ	
pGEMEX-oligo2/3	SCG	CCG AAT TCT TGA TGA GGC AGT GAT GCC GAA	TCT	TGA	TGA	355	AGT	GAT	325	GAA	AAG	CTT	GGC	Ü	
	၁၅၅	TTA	AGA	ACT	ACT	CCG	T.	CTA	טטט	Į.	000 000 640 000 This This 250	K K			

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GCA	GCA	GCA	GCA	
CAT	CAT	-	-	
SCG	CCG	CCG	ಖ್ಯ	
CGG	CGG	CGG		
	ATT			
	GGA			
TCA	TCA	TCA		
	TCA			
၁၁၅				
ACT				
ATC	ATC			
GGC	GGC			
$_{ m TTC}$	TTC		ATG	
CTT	CTT		TAG	
AAG	AAG		CTC	
GCC	GCC			
9 90		CGG	CGG	
Clone 1:	Clone 2:	Clone 3:	pGEMEX: cca	

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GAA	GAA	
CAT CAG GAA	CAG GAA	
CAT	CAT	
SCA TCA CTG CCT	$_{\rm CCT}$	
CTG	CTG	
TCA	SCA TCA	
GCA	GCA	

CTT CTT CTT AAG AAG

CTG CTG GGC TIC GGC GGC $_{
m TTC}$ TTC

CTG CAT AAG CAT CAT CAT

TCA CTG CCT CAT CAG GAA

GCA TCG GCA TCG TCG TTT LLI TTT

CTG CAA AGC AGC AGC CAA CAA CTG CGC

GGC CGC GGC

PGEMEX Clone 1: Clone 2: Clone 3: